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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/028,051

DATE: 01/24/2002
TIME: 15:04:36

Input Set : N:\Crf3\RULE60\10028051.txt
Output Set: N:\CRF3\01242002\J028051.raw

SEQUENCE LISTING

C--> 5 (1) GENERAL INFORMATION:

(i) APPLICANT: Luyten, Frank P.
Hoang, Bang
Moos, Jr., Malcolm
Wang, Shouwen

C--> 12 (ii) TITLE OF INVENTION: ISOLATION AND USE OF TISSUE
GROWTH INDUCING FRZB PROTEIN

15 (iii) NUMBER OF SEQUENCES: 23

17 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear
(B) STREET: 620 Newport Center Drive, 16th Floor
(C) CITY: Newport Beach
(D) STATE: CA
(E) COUNTRY: U.S.A.
(F) ZIP: 92660

25 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5

31 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/10/028,051
(B) FILING DATE: 19-Dec-2001
(C) CLASSIFICATION:

36 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/729,452
(B) FILING DATE:

42 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bartfeld, Neil S
(B) REGISTRATION NUMBER: 39,901
(C) REFERENCE/DOCKET NUMBER: NIH133.001A

47 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-235-8550
(B) TELEFAX: 619-235-0176
(C) TELEX:

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

61 (ix) FEATURE:

ENTERED

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63 (A) NAME/KEY: Coding Sequence

64 (B) LOCATION: 256...1230

65 (D) OTHER INFORMATION:

68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

70	AATAGATGCC GCGGCCCCAG AAGTCTTAGA CGTCGGGAAA GAGCAGCCCG AGAGGCAGGG	60
71	GCGGCGGCGG CTGGCGCTCG GCGCAGCTTT TGGGACCCCA TTGAGGGAAT TTGATCCAAG	120
72	GAAGCTGTGA GATTGCCGGG GGAGGAGAAG CTCCCATATC ATTGTGTCCA CTTCCAGGGC	180
73	GGGGAGGAGG AAACGGCGGA GCGGGCCTCT CGGCGTTCTC CGCACTGCTG CACCCTGCCC	240
74	CATCCTGCCG AGATC ATG GTC TGC GGG AGC CGA GGC GGG ATG CTG CTG CTG	291
75	Met Val Cys Gly Ser Arg Gly Gly Met Leu Leu Leu	
76	1 5 10	
78	CCG GCC GGG CTA CTC GCC CTG GCT GCG CTC TGC CTG CTC CGC GTG CCC	339
79	Pro Ala Gly Leu Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro	
80	15 20 25	
82	GGA GCG CGG GCG GCC GCC TGT GAG CCC GTT CGC ATT CCC CTG TGC AAG	387
83	Gly Ala Arg Ala Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys	
84	30 35 40	
86	TCC CTG CCC TGG AAC ATG ACT AAG ATG CCC AAC CAC CTG CAC CAC AGC	435
87	Ser Leu Pro Trp Asn Met Thr Lys Met Pro Asn His Leu His His Ser	
88	45 50 55 60	
90	ACC CAG GCC AAC GCC ATC CTG GCC ATC GAG CAG TTC GAA GGT CTG CTG	483
91	Thr Gln Ala Asn Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu	
92	65 70 75	
94	GGC ACC CAC TGC AGC CCG GAT CTG CTC TTC TTC CTC TGT GCT ATG TAC	531
95	Gly Thr His Cys Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr	
96	80 85 90	
98	GCG CCC ATC TGC ACC ATT GAC TTC CAG CAC GAG CCC ATC AAG CCC TGC	579
99	Ala Pro Ile Cys Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys	
100	95 100 105	
102	AAG TCT GTG TGC GAG CGG GCC CGG CAG GGC TGT GAG CCC ATC CTC ATC	627
103	Lys Ser Val Cys Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile	
104	110 115 120	
106	AAG TAC CGC CAC TCG TGG CCG GAA AGC CTG GCC TGC GAG GAG CTG CCA	675
107	Lys Tyr Arg His Ser Trp Pro Glu Ser Leu Ala Cys Glu Glu Leu Pro	
108	125 130 135 140	
110	GTA TAT GAC CGC GGC GTG TGC ATC TCT CCG GAG GCC ATC GTC ACT GCC	723
111	Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala	
112	145 150 155	
114	GAC GGA GCC GAT TTT CCT ATG GAT TCC AGT AAT GGA AAC TGT AGA GGA	771
115	Asp Gly Ala Asp Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly	
116	160 165 170	
118	GCA AGC AGT GAA CGC TGC AAA TGT AAA CCA GTC AGA GCT ACA CAG AAG	819
119	Ala Ser Ser Glu Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys	
120	175 180 185	
122	ACC TAT TTC CGA AAC AAT TAC AAC TAT GTC ATT CGG GCT AAA GTT AAA	867
123	Thr Tyr Phe Arg Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys	
124	190 195 200	
126	GAA ATA AAG ACC AAG TGT CAT GAT GTG ACT GCA GTA GTG GAG GTG AAG	915
127	Glu Ile Lys Thr Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys	

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128	205	210	215	220	
130	GAG ATT TTA AAG GCT TCT CTG GTA AAC ATT CCA AGG GAA ACT GTG AAC	963			
131	Glu Ile Leu Lys Ala Ser Leu Val Asn Ile Pro Arg Glu Thr Val Asn				
132	225	230	235		
134	CTT TAT ACC AGC TCT GGC TGC CTG TGT CCT CCA CTT AAC GTT AAT GAG	1011			
135	Leu Tyr Thr Ser Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu				
136	240	245	250		
138	GAG TAT CTC ATC ATG GGC TAC GAA GAT GAA GAG CGC TCC AGA TTA CTG	1059			
139	Glu Tyr Leu Ile Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu				
140	255	260	265		
142	TTG GTA GAA GGT TCT ATT GCT GAG AAA TGG AAG GAT CGA CTT GGT AAA	1107			
143	Leu Val Glu Gly Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys				
144	270	275	280		
146	AAA GTT AAG CGG TGG GAT ATG AAG CTC CGT CAT CTT GGA CTG AAT ACA	1155			
147	Lys Val Lys Arg Trp Asp Met Lys Leu Arg His Leu Gly Leu Asn Thr				
148	285	290	295	300	
150	AGT GAT TCT AGC CAT AGT GAT TCC ACT CAG AGT CAG AAG CCT GGC AGG	1203			
151	Ser Asp Ser Ser His Ser Asp Ser Thr Gln Ser Gln Lys Pro Gly Arg				
152	305	310	315		
154	AAT TCT AAC TCC CGG CAA GCA CGC AAC TAAATCCTGA AATGCAGAAA ATCCTCA	1257			
155	Asn Ser Asn Ser Arg Gln Ala Arg Asn				
156	320	325			
158	GTGGACTTCC TATTAAGACT TGCATTGCTG GACTAGCAAA GGCAAATTGC ACTATTGCAC	1317			
159	GTCATAGTCT ATTTTITAGC CACAAAAATC AGGTGGTAAC TGATATTACT TCTATTTTTT	1377			
160	CTTTTGTTTT CTGCTTTTCT CCTTCCCCCA TTCCCTTTTT TGTGGTCTGA GTACAGATCC	1437			
161	TTAAATATAT TATATGTATT CTATTTTCACT AATCATGGGA AAACGTGTTCT TTGCAATAAT	1497			
162	AATAAATTAA ACATGTTGAT ACCAGGGCCT CTTTGCTGGA GTAAATGTTA ATTTGCTGTT	1557			
163	CTGCACCCAG ATTGGGAATG CAATATTGGA TGCAAAGAGA GATTTCTGGT ATACAGAGAA	1617			
164	AGCTAGATAG GCTGTAAAGC ATACTTTGCT GATCTAATTA CAGCCTCATT CTTGCATGCC	1677			
165	TTTTGGCATT CTCCTCACGC TTAGAAAGTT CTAAATGTTT ATAAAGGTAA AATGACAGTT	1737			
166	TGAAATCAAA TGCCAACAGG CAGAGCAATC AAGCACCAGG AAGCATTTAT GAAGAAATGA	1797			
167	CACATGAGAT GAATTATTG CAAGATTGGC AGGAAGCAAA ATAAATAGCA TTAGGAGCTG	1857			
168	GGGATAGAGC ATTTTGCTG ACTGAGAAGC ACAACTGAAG CTAGTAGCTG TTGGGGTGTT	1917			
169	AACAGCAGCA TTTTCTTTTT GACGATACAT TTGTTTGTCT GTGAATATAT TGATCAGCAT	1977			
170	TAGAGCAGTG GATTGTGACC AGACATCAGG TGTTATCAGC ATAGCTCTGT TTAATTTGCT	2037			
171	TCCTTTTAGA TGAACGCATT GGTGTCTTTT TTTTCTTCTT TTAATAATAA TCTCCCTTGC	2097			
172	TGCATTTGAC CAGGAAAAGA AAGCATATAT GCATGTGCAC CGGGCTGTTA TTTTAAAGAT	2157			
173	ATGTAGCTCT ATAAACGCT ATAGTCAAAA GATGGTAAAA TGTGCAAGAT TCTGGGTGTG	2217			
174	TGTATTAATG TGTGTGTGTC CGCATACACT CACACTCAAG CTGAAGTGAA CGACAGGCCT	2277			
175	GTGCACTGGC CTGCACTTTA TCATTTGGAT TTGTGCTGTT TAATGCTCAG TAAAATATGC	2337			
176	TTAATAAAAAG GAAAAAAAAA AAAAAAAAAA AAAAAA	2374			

178 (2) INFORMATION FOR SEQ ID NO: 2:

180 (i) SEQUENCE CHARACTERISTICS:

181 (A) LENGTH: 325 amino acids

182 (B) TYPE: amino acid

183 (C) STRANDEDNESS: single

184 (D) TOPOLOGY: linear

186 (ii) MOLECULE TYPE: protein

187 (v) FRAGMENT TYPE: internal

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189 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
191 Met Val Cys Gly Ser Arg Gly Gly Met Leu Leu Leu Pro Ala Gly Leu
192 1 5 10 15
193 Leu Ala Leu Ala Ala Leu Cys Leu Leu Arg Val Pro Gly Ala Arg Ala
194 20 25 30
195 Ala Ala Cys Glu Pro Val Arg Ile Pro Leu Cys Lys Ser Leu Pro Trp
196 35 40 45
197 Asn Met Thr Lys Met Pro Asn His Leu His His Ser Thr Gln Ala Asn
198 50 55 60
199 Ala Ile Leu Ala Ile Glu Gln Phe Glu Gly Leu Leu Gly Thr His Cys
200 65 70 75 80
201 Ser Pro Asp Leu Leu Phe Phe Leu Cys Ala Met Tyr Ala Pro Ile Cys
202 85 90 95
203 Thr Ile Asp Phe Gln His Glu Pro Ile Lys Pro Cys Lys Ser Val Cys
204 100 105 110
205 Glu Arg Ala Arg Gln Gly Cys Glu Pro Ile Leu Ile Lys Tyr Arg His
206 115 120 125
207 Ser Trp Pro Glu Ser Leu Ala Cys Glu Glu Leu Pro Val Tyr Asp Arg
208 130 135 140
209 Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr Ala Asp Gly Ala Asp
210 145 150 155 160
211 Phe Pro Met Asp Ser Ser Asn Gly Asn Cys Arg Gly Ala Ser Ser Glu
212 165 170 175
213 Arg Cys Lys Cys Lys Pro Val Arg Ala Thr Gln Lys Thr Tyr Phe Arg
214 180 185 190
215 Asn Asn Tyr Asn Tyr Val Ile Arg Ala Lys Val Lys Glu Ile Lys Thr
216 195 200 205
217 Lys Cys His Asp Val Thr Ala Val Val Glu Val Lys Glu Ile Leu Lys
218 210 215 220
219 Ala Ser Leu Val Asn Ile Pro Arg Glu Thr Val Asn Leu Tyr Thr Ser
220 225 230 235 240
221 Ser Gly Cys Leu Cys Pro Pro Leu Asn Val Asn Glu Glu Tyr Leu Ile
222 245 250 255
223 Met Gly Tyr Glu Asp Glu Glu Arg Ser Arg Leu Leu Leu Val Glu Gly
224 260 265 270
225 Ser Ile Ala Glu Lys Trp Lys Asp Arg Leu Gly Lys Lys Val Lys Arg
226 275 280 285
227 Trp Asp Met Lys Leu Arg His Leu Gly Leu Asn Thr Ser Asp Ser Ser
228 290 295 300
229 His Ser Asp Ser Thr Gln Ser Gln Lys Pro Gly Arg Asn Ser Asn Ser
230 305 310 315 320
231 Arg Gln Ala Arg Asn
232 325
234 (2) INFORMATION FOR SEQ ID NO: 3:
236 (i) SEQUENCE CHARACTERISTICS:
237 (A) LENGTH: 1484 base pairs
238 (B) TYPE: nucleic acid
239 (C) STRANDEDNESS: single
240 (D) TOPOLOGY: linear

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242 (ix) FEATURE:
244 (A) NAME/KEY: Coding Sequence
245 (B) LOCATION: 208...1182
246 (D) OTHER INFORMATION:
249 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

251	CGGGGCCTGG	GCGGSAGGGG	CGGTGGCTGG	AGCTCGGTAA	AGCTCGTGGG	ACCCCATTTGG	60
252	GGAATTTGA	TCCAAGGAAG	CGGTGATTGC	CGGGGGAGGA	GAAGCTCCCA	GATCCTTGTG	120
253	TCCACTTGCA	GCGGGGGAGG	CGGAGACGCG	GAGCGGGCCT	TTTGGCGTCC	ACTGCGCGGC	180
254	TGCACCCTGC	CCCATCCTGC	CGGGATC	ATG	GTC	TGC	234
255				Met	Val	Cys	
256				1		5	
258	CTG	CTG	CTG	CGG	GCC	GGG	282
259	Leu	Leu	Leu	Arg	Ala	Gly	
260	10			15		20	
262	CGG	GTG	CCC	GGG	GCT	CGG	330
263	Arg	Val	Pro	Gly	Ala	Arg	
264				30		35	
266	CTG	TGC	AAG	TCC	CTG	CCC	378
267	Leu	Cys	Lys	Ser	Leu	Pro	
268				45		50	
270	CAC	CAC	AGC	ACT	CAG	GCC	426
271	His	His	Ser	Thr	Gln	Ala	
272				60		65	
274	GGT	CTG	CTG	GGC	ACC	CAC	474
275	Gly	Leu	Leu	Gly	Thr	His	
276				75		80	
278	GCC	ATG	TAC	GCG	CCC	ATC	522
279	Ala	Met	Tyr	Ala	Pro	Ile	
280	90			95		100	
282	AAG	CCC	TGT	AAG	TCT	GTG	570
283	Lys	Pro	Cys	Lys	Ser	Val	
284				110		115	
286	ATA	CTC	ATC	AAG	TAC	CGC	618
287	Ile	Leu	Ile	Lys	Tyr	Arg	
288				125		130	
290	GAG	CTG	CCA	GTG	TAC	GAC	666
291	Glu	Leu	Pro	Val	Tyr	Asp	
292				140		145	
294	GTT	ACT	GCG	GAC	GGA	GCT	714
295	Val	Thr	Ala	Asp	Gly	Ala	
296				155		160	
298	TGT	AGA	GGG	GCA	AGC	AGT	762
299	Cys	Arg	Gly	Ala	Ser	Ser	
300	170			175		180	
302	ACA	CAG	AAG	ACC	TAT	TTC	810
303	Thr	Gln	Lys	Thr	Tyr	Phe	
304				190		195	
306	AAA	GTT	AAA	GAG	ATA	AAG	858
307	Lys	Val	Lys	Glu	Ile	Lys	

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10028051.txt

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L:5 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:12 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:32 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12